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DETECTION OF *ANAPLASMA BOVIS* IN AN UNDESCRIBED TICK SPECIES COLLECTED FROM THE EASTERN ROCK SENGI *ELEPHANTULUS MYURUS*

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ABSTRACT: Ticks are important vectors of numerous pathogens causing illness, fatalities, and economic loss worldwide. Infectious disease episodes are increasing, and novel tick-borne pathogens are described frequently. Identification of novel reservoir hosts and vectors of tick-borne pathogens is essential if control measures are to be successful. In South Africa, the eastern rock sengi, *Elephantulus myurus*, hosts a number of tick species of veterinary importance. Despite this, there remains a paucity of information regarding the tick fauna of this species, the pathogen associations of ticks that it hosts, and its role as a reservoir host of tick-borne pathogens. The current study documents the tick fauna of *E. myurus* and sympatric small mammal species in Limpopo Province, South Africa. The pathogen associations of ticks hosted by elephant shrews were also investigated by PCR screening of engorged nymphs for a broad range of bacterial and protozoan tick-borne infections, including *Borrelia burgdorferi* sensu lato and members of Apicomplexa and the order Rickettsiales. There were marked differences in tick species and abundance among host species. *Elephantulus myurus* was heavily, and predominantly, parasitized by an as-yet undescribed tick species that we identify as *Rhipicephalus* sp. near *warburtoni*. PCR and sequence analysis revealed the presence of *Anaplasma bovis* in this tick species, which may have consequences for livestock production and conservation efforts in the area where this tick species occurs.

Ticks are vectors of some of the most important pathogens affecting humans and livestock throughout the world (Jongejan and Uilenberg, 2005). Recently, the number of human infectious disease episodes attributed to tick-borne pathogens has increased (Spach et al., 1993; Jensenius et al., 2003; Randolph, 2004), and novel tick-borne pathogens are being discovered regularly (Parola and Raoult, 2001). Economic losses to agriculture through mortality and the treatment of tick-borne infections are also substantial (Kivaria, 2006). In order to identify the risk posed to animal and human health, and as a starting point for control, it is important to identify novel reservoirs and vectors of emerging infectious diseases.

Elephant shrews, or sengis, of the Macroscelidae are hosts for the immature stages of approximately 27 species of ixodid ticks in Africa (Fourie et al., 1995). Eastern rock sengis, *Elephantulus myurus*, are of particular interest because they host large numbers of the immature stages of 3 tick species that transmit toxins causing paralysis in domestic animals. *Ixodes rubicundus* is responsible for numerous annual mortalities of sheep in South Africa (Spickett and Heyne, 1988). *Rhipicentor nuttalli* causes paralysis in dogs (Norval and Colborne, 1985), while *Rhipicephalus warburtoni* has been implicated in the paralysis of goats (Fourie et al., 1988). Despite the potential for *E. myurus* to host ticks of medical and veterinary importance, there remains a paucity of information regarding the tick associations of this species. Moreover, the vector competence and disease associations of many of the tick species that infest *E. myurus* have not been established (Walker et al., 2000).

Rodents are important hosts for immature ixodid ticks across the world (Sonenshine, 1991), but the limited data available from locations in South Africa suggest that elephant shrews carry much larger tick loads than sympatric rodent species (MacLeod, 1970; Colbo and MacLeod, 1976; Fourie et al., 1992). The reason for this disparity in tick loads between small mammal species is unclear, and the extent of this phenomenon is currently unknown.

The present study aims to document the tick fauna of the eastern rock sengi, *E. myurus*, and sympatric small mammal species in Limpopo Province, South Africa. We also aim to assess the potential for elephant shrews to act as reservoir hosts of tick-borne pathogens by screening engorged ticks collected from these animals for a wide range of bacterial and protozoan pathogens using PCR.

MATERIALS AND METHODS

Small mammals were trapped across 20 consecutive nights between 24 April and 13 May 2009 at Goro Game Reserve (23°00′12″S, 29°26′03″E), located in the Soutpansberg mountain range, Limpopo Province, South Africa. Two-hundred Sherman live traps, baited with an oats, peanut butter, and sardine mix, were deployed in lines at 10-m intervals on rocky outcrops. Depending on the terrain, either 2 trap lines of 100 traps or 4 trap lines of 50 traps were set in parallel rows 10 m apart. All traps were set after 1600 hr and collected before 0800 hr the next day. Animals were identified to species, and their sex, age, and body mass were recorded. The body of each individual was searched for ticks, and particular attention was given to the ear margins, legs, and the base of the tail, where ticks aggregated. The rest of the body was searched by back-combing the fur. All ticks were removed using fine-tipped forceps and placed in 70% ethanol, and the animals were released. Ticks were identified to species or species group by I.G.H. using descriptions provided by Theiler (1961), Walker et al. (2000), and Apanaskevich et al. (2007) and by comparison with reference material. Developmental stage was recorded as larva, nymph, or adult. The study was conducted with the ethical approval of the Animal Care and Use Committee, University of Pretoria, under permit number EC015-09.

The correlation of sex, body size, and their interaction on total tick loads of *E. myurus* and *Micaelamys namaquensis* was investigated using generalized linear models (GLMs) with a negative binomial error distribution and a log link function. To avoid the confounding effect of host age on body mass and immune status, all models were conducted on a subset of data containing adults only. Analyses were performed using the glm.nb procedure in package MASS in the R software package available under GNU license at http://www.r-project.org.

Five engorged nymphs collected from each *E. myurus* individual were placed in 2-ml Sure-Lock microcentrifuge tubes, and 0.5-ml aliquots of 1.25% ammonia solution were added. The nymphs were macerated using a single sterile pipette tip, and DNA was extracted as previously described (Bown et al., 2003). Ten-microliter samples of extract from each of the 5 ticks were then combined to give a 50-μl pooled sample representing a single host animal.

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TABLE I. Total abundances and mean infestations (±1 standard error) of tick species or species group parasitizing small mammals.

	M. namaquensis (n = 172)	*E. myurus* (n = 57)	*Acomys spinosissimus* (n = 16)	*Aethomys chrysophilus* (n = 7)
Rhipicephalus sp. near *warburtoni*				
Larvae	3 (0.017 ± 0.010)	21,645 (379.737 ± 33.843)	0	0
Nymphs	0	1,084 (19.018 ± 1.335)	0	0
Total	3 (0.017 ± 0.010)	22,729 (398.754 ± 33.962)	0	0
*Rhipicephalus simus/follis**				
Larvae	74 (0.430 ± 0.715)	2 (0.035 ± 0.025)	2 (0.125 ± 0.085)	2 (0.286 ± 0.286)
Nymphs	77 (0.448 ± 0.092)	1 (0.018 ± 0.018)	5 (0.313 ± 0.176)	3 (0.429 ± 0.297)
Total	151 (0.878 ± 0.126	3 (0.053 ± 0.030)	7 (0.438 ± 0.182)	5 (0.714 ± 0.565)
Rhipicephalus lunulatus				
Larvae	0	0	0	0
Nymphs	2 (0.012 ± 0.008)	1 (0.018 ± 0.018)	0	2 (0.286 ± 0.286)
Total	2 (0.012 ± 0.008)	1 (0.018 ± 0.018)	0	2 (0.286 ± 0.286)
*Haemaphysalis elliptica**				
Larvae	0	0	0	0
Nymphs	4 (0.023 ± 0.142)	0	0	1 (0.143 ± 0.143)
Total	4 (0.023 ± 0.142)	0	0	1 (0.143 ± 0.143)
*Rhipicentor nuttalli/bicornis**				
Larvae	0	1 (0.018 ± 0.018)	0	0
Nymphs	0	5 (0.088 ± 0.072)	0	0
Total	0	6 (0.105 ± 0.074)	0	0
Unknown larvae	17 (0.099 ± 0.049)	0	1 (0.063 ± 0.063)	0
Total				
Larvae	94 (0.547 ± 0.086)	21,648 (379.790 ± 33.843)	3 (0.188 ± 0.101)	2 (0.286 ± 0.286)
Nymphs	83 (0.483 ± 0.094)	1,091 (19.140 ± 1.331)	5 (0.313 ± 0.176)	6 (0.857 ± 0.705)
Combined	177 (1.029 ± 0.135)	22,739 (398.930 ± 33.952)	8 (0.500 ± 0.224)	8 (1.143 ± 0.986)

* Ticks identified only to species group because of current classification ambiguity.

To assess the reservoir potential of *E. myurus* for tick-borne pathogens, a range of non-specific diagnostic tests was used. Pooled tick samples were tested for the presence of *Borrelia burgdorferi* sensu lato, species of Apicomplexa, (including *Babesia* spp.), and for the order Rickettsiales (including species of *Ricksettsia*, *Anaplasma*, and *Ehrlichia*) by PCR as described previously (Pancholi et al., 1995; Courtney et al., 2004; Simpson et al., 2005). Positive samples were identified via electrophoretic resolution of PCR products on a 1.0% agarose gel stained with ethidium bromide and examined under UV light. All PCRs included negative controls in a ratio of 1 to 5 and positive controls. Amplification products were purified using Qiaquick kit (Qiagen, Valencia, California), and sequences were determined using a commercial sequencing service (Macrogen, Seoul, Korea). Successfully sequenced amplification products were used to search for other closely related sequences using the NCBI nucleotide BLAST database, and other known species within the genus were included in the analysis. Sequences were aligned and compared using BioEdit v.7.0.9©.

RESULTS

Tick data

In total, 172 Namaqua rock mice (*Micaelamys namaquensis*), 57 eastern rock elephant shrews (*Elephantulus myurus*), 16 spiny mice (*Acomys spinosissimus*), and 7 red rock rats (*Aethomys chrysophilus*) were caught across 2,600 trap nights. Marked differences were evident among the tick fauna of each host species. *Elephantulus myurus* was heavily parasitized, hosting tick abundances many orders of magnitude greater than other hosts. Altogether, 22,739 ticks (21,648 larvae and 1,091 nymphs) (Table I) were collected from *E. myurus*, the vast majority of which (22,729, 99.95%) belonged to an undescribed tick species that we have designated as *Rhipicephalus* sp. near *warburtoni*. This tick was remarkably abundant on *E. myurus*, with mean infestations of 379.7 ± 33.8 larvae and 19.1 ± 1.3 (±SE) nymphs, but it was virtually absent from sympatric rodent species. Although in low numbers, ticks from the *Rhipicentor nuttalli/bicornis* group were only found on *E. myurus*. Small numbers of ticks belonging to the *Rhipicephalus simus/follis* group were collected from all host species but were present on *E. myurus* at lower abundances than on the other small mammals. Small numbers of *Rhipicephalus lunulatus* and ticks belonging to the *Haemaphysalis elliptica* group were also present on hosts. None of the characteristics recorded, i.e., sex, mass, and their interactions, significantly affected tick loads on *E. myurus* or *M. namaquensis* (Table II). In addition, an incidental collection of ticks found that questing on the tips of grass within Goro Game Reserve yielded 10 males and 8 females of *Rhipicephalus appendiculatus* and 5 males and 7 females of *R.* sp. near *warburtoni*.

Pathogen detection

Of the 57 tick pools tested, none was positive for *B. burgdorferi* sensu lato or any species of Apicomplexa. Four tick pools of *R.* sp. near *warburtoni* tested positive for the presence of Rickettsiales. Two of the 4 amplification products were successfully sequenced and produced 2 identical full-length sequences of 203 base pairs. The remaining 2 amplification products produced mixed signals and were not included in further analyses. The 2 sequences successfully recovered were identical to sequences of the 16S gene

TABLE II. Generalized linear models investigating the effect of sex and mass on tick loads of *Elephantulus myurus* and *Micaelamys namaquensis*. Parameter coefficients ± 1 standard error; z-values and associated *P*-values are presented.

	β coefficient	SE	z-value	*P*-value
E. myurus (n = 56)				
Intercept	5.139	1.252	4.104	0.000*
Sex	−0.435	1.526	−0.285	0.775
Mass	0.019	0.024	0.763	0.446
Sex × mass	0.006	0.030	0.189	0.850
M. namaquensis (n = 148)				
Intercept	−0.431	1.149	−0.376	0.707
Sex	−0.421	1.610	−0.262	0.793
Mass	0.010	0.027	0.394	0.694
Sex × mass	0.014	0.039	0.364	0.716

* Indicates significance at the $P < 0.001$ level.

of *Anaplasma bovis* isolated from *Haemaphysalis longicornis* ticks in South Korea, domestic livestock in China, from an unknown host in South Africa, and 2 uncultured *Anaplasma* spp. from Japan. The next most closely related sequence was a strain of *A. bovis* isolated from an eastern cottontail rabbit in the United States (99.5%). The most closely related strains not belonging to *A. bovis* were *Anaplasma platys* and *Anaplasma phagocytophilum* (99.0%), while *Anaplasma marginale* and *Anaplasma ovis* were 96.0% related.

DISCUSSION

Identification of tick species

The taxonomic status and specific identification of the tick species collected from eastern rock sengis and other small mammals in this study are problematic. By making use of the morphology of immature stages, Walker et al. (2000) identified 6 species groups within *Rhipicephalus*. The *Rhipicephalus pravus* group contains 6 species, including *R. warburtoni* sensu stricto and a further 2 species that have not been described (*Rhipicephalus* sp. near *pravus* and *Rhipicephalus* sp. near *punctatus*). Based on the morphological similarities of the larvae, nymphs, and adults of this species to each other and to those of other tick species in the *R. pravus* group, we now add another undescribed species to the group. Until a thorough taxonomic study is conducted, we have chosen to name this tick *R.* sp. near *warburtoni*, due to its close morphological similarity to *R. warburtoni* sensu stricto, as described and illustrated by Walker et al. (2000). With the exception of *Rhipicephalus oculatus*, the immature stages of the ticks within the *R. pravus* group feed on sengis (Walker et al., 2000). Because it is extremely difficult to distinguish between the immature stages of the *Rhipicephalus simus* and *Rhipicephalus follis* groups (Walker et al., 2000), as well as those of *Rhipicentor bicornis* and *Rhipicentor nuttalli* (Theiler, 1961), and of the *Haemaphysalis elliptica* group (Apanaskevich et al., 2007), the immature stages were designated to the appropriate group.

Pathogen detection

There are currently no known pathogen associations of *R.* sp. near *warburtoni*; therefore, the present study provides the first record of the presence of *A. bovis* in this tick. *Anaplasma bovis* (previously *Ehrlichia bovis*) was first described in 1936 during transmission experiments involving *Hyalomma* from Iranian and French cattle (Donatien and Lestoquard, 1936). Its presence in South Africa was confirmed in 1937 in blood and lymph node smears from cattle on which adult *Rhipicephalus appendiculatus* collected in Limpopo Province were allowed to feed (De Kock et al., 1937). Since then, it has been isolated from deer, goats, and buffalo, but most commonly domestic cattle in Africa, Brazil, Japan, and the Middle East (Uilenberg, 1997; Kawahara et al., 2006; Santos and Cavalho, 2006; Ooshiro et al., 2008). It has also been recovered from *Haemaphysalis* spp. ticks in Korea and cottontail rabbits, *Sylvilagus floridanus*, in North America (Goethert and Telford, 2003; Kim et al., 2003). The bacteria infect monocytes within the blood of their hosts, resulting in debility, fever, anorexia, and up to 40% mortality of cattle in some cases (Stewart, 1993; Santos and Carvalho, 2006). Adults of *R. warburtoni* sensu stricto feed on scrub hares, *Lepus saxatilis*, as well as on a range of large mammals, including domestic stock and wild ungulates (Walker et al., 2000). If adults of *R.* sp. near *warburtoni* have a similar host preference that includes domestic stock, and are competent vectors of *A. bovis*, the discovery of *A. bovis* in this tick could have important implications for livestock production and conservation.

Because only engorged nymphs were tested for the presence of *A. bovis*, it is unclear whether *E. myurus* was the reservoir host of this pathogen or if the nymphs had acquired infection while feeding on an alternative host as larvae. Given the virtual absence of this tick on the other small mammal hosts in the current study, it is unlikely that they were the source of infection. Goethert and Telford (2003) found that *Haemaphysalis leporispalustris* ticks could maintain enzootic infections of *A. bovis* in cottontail rabbits in the United States and suggested that leporids may be a natural reservoir host of this pathogen. In the present study, it is possible that *E. myurus* were simply feeding nymphs that had acquired the infection from scrub hares while feeding as larvae. Moreover, while *A. bovis* DNA was detected in engorged nymphs of *R.* sp. near *warburtoni*, we cannot assume that this tick species is a vector until transmission experiments are conducted using live animal models.

The geographic distribution of *R. warburtoni* sensu stricto is confined to the southwestern and central regions of Free State Province, South Africa. Within the latter region, large numbers of larvae and nymphs of this tick are found on scrub hares and eastern rock sengis (Horak and Fourie, 1991; Fourie et al., 2005), while adults are present on scrub hares and domestic and wild ruminants (Walker et al., 2000). In Limpopo Province, only the larvae and nymphs of *R.* sp. near *warburtoni* have been collected from eastern rock sengis, and the hosts of the adults are unknown, but may be scrub hares. Although surveys have been conducted on scrub hares in Limpopo Province, no individuals of *R. warburtoni* sensu stricto or *R.* sp. near *warburtoni* have been found on these animals (Horak et al., 1993), whereas other ticks belonging to the *R. pravus* group have. Therefore, the importance of scrub hares as hosts of *R.* sp. near *warburtoni* and their reservoir status for *A. bovis* are currently unknown.

Tick–host relationships

There were marked differences in the tick fauna of the host species examined in the present study, and tick loads encountered on *E. myurus* were much higher than those present on rodents, as

reported elsewhere (MacLeod, 1970; Colbo and MacLeod, 1976; Fourie et al., 1992). Whereas the underlying cause is currently unknown, there are a number of mechanisms that could explain the differences in parasitism between these hosts. *Elephantulus myurus* is a solitary species (Ribble and Perrin, 2005), while *M. namaquensis* is communal, living in family groups of up to 10 individuals (Smithers, 1971; Choate, 1972). Thus, it may be expected that an increase in sociality could lead to increased transmission rates for direct-transmitted parasites (Cote and Poulin, 1995). Social animals can also benefit from allogrooming or the dilution of ectoparasites amongst potential hosts, thus inducing reduced levels of parasitism (Marshall, 1981; Bordes et al., 2007; Hillegass et al., 2008). Differences in activity patterns may also play a role. *Micaelamys namaquensis* is nocturnal (Fleming and Nicolson, 2004), while *E. myurus* is active throughout the day and night (Ribble and Perrin, 2005). Ticks may also exhibit daily detachment rhythms (Rechav, 1978; Du Toit et al., 1994b) and may have daily activity patterns while questing (Semtner and Hair, 1973; Belozerov, 1982; Madden and Madden, 2005). Thus, differences in the daily movements of hosts will determine the frequency with which they encounter ticks. Similarly, differences in home range size and mobility (Morand et al., 2004) or microhabitat selection may influence tick contact rates. It has been suggested that *M. namaquensis* may use trees as nest sites (Skinner and Chimimba, 2005); in this case, they would not encounter ticks questing on vegetation or from the soil surface as frequently as strictly ground-dwelling species such as *E. myurus*. Ticks also display different patterns of appetence behavior (Fourie et al., 1993), may be attracted to specific chemical compounds associated with hosts (Rechav, 1978), or to ticks that have already attached (Norval, Perry, and Young, 1992). Host immunity could also contribute to differences in tick load; some species of small mammals develop immunity to ticks (Dizij and Kurtenbach, 1995), although others, including eastern rock sengis, may not (Du Toit et al., 1994a).

Rhipicentor nuttalli has been recovered previously from *E. myurus* in the northern provinces of South Africa (Fourie et al., 2002, 2005). *Elephantulus myurus* is thought to be an important host for the immature stages of *Rh. nuttalli* (Fourie et al., 2002). Although quite rare, this tick is potentially important because it produces a toxin that causes paralysis in domestic dogs (Perchman, 1976; Norval and Colborne, 1985). To our knowledge, immature stages of *R. lunulatus* and of the *R. simus/follis* group have not been reported on *E. myurus* previously. *Rhipicephalus lunulatus* is the suspected vector of *Babesia trautmanni*, the causative agent of piroplasmosis in pigs (Tendeiro, 1952, cited in Walker et al., 2000) and has been associated with toxic paralysis in lambs and calves (Theiler, 1962; Lawrence and Norval, 1979). The role of *E. myurus* in the life cycle of this tick species is unknown, but in the current study, only a single nymph was recovered. *Rhipicephalus simus* transmits *Anaplasma marginale* and *Anaplasma centrale*, the causative agents of bovine anaplasmosis (Norval, Peter, and Meltzer, 1992; Jongejan and Uilenberg, 2005), and it is also a vector of *Rickettsia conorii*, the cause of Mediterranean spotted fever in humans (Gear, 1992). However, compared to the 3 rodent species examined in this study, *E. myurus* is a poor host for the larvae and nymphs of *R. simus* and is unlikely to play an important role in the life cycle of this tick. Nothing is known about the pathogen associations of *R. follis* (Walker et al., 2000).

Future work should focus on the screening of blood from elephant shrews in order to identify the natural reservoir of *A. bovis* in this system and on the description of *R.* sp. near *warburtoni*. The ability of *R.* sp. near *warburtoni* to transmit *A. bovis* should also be investigated. The present study documents the presence of *A. bovis* DNA in a previously unknown species, *R.* sp. near *warburtoni*, for the first time, providing much needed information regarding the tick-pathogen associations of small mammals in Africa. The study also highlights the importance of continued surveillance for novel wildlife reservoirs and vectors of tick-borne pathogens.

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